Mapping the transcriptional regulatory elements in the genome of hESC

Grant Award Details

Mapping the transcriptional regulatory elements in the genome of hESC

Grant Type: SEED Grant

Grant Number: RS1-00292

Investigator:

Name:	Bing Ren
Institution:	Ludwig Institute for Cancer Research
Type:	PI

Human Stem Cell Use: Embryonic Stem Cell

Award Value: $653,823

Status: Closed

Progress Reports

Reporting Period: Year 2

View Report

Reporting Period: NCE

View Report

Grant Application Details

Application Title: Mapping the transcriptional regulatory elements in the genome of hESC

Public Abstract:

The human embryonic stem cells (hESC) have the remarkable potential to replicate themselves indefinitely and differentiate into virtually any cell type under appropriate environmental conditions. They accomplish this through regulating the production of a unique set of proteins in the cells, a process known as gene regulation. While the genes encoding these stem cell proteins have been largely identified over the years, the mechanisms of gene regulation are not yet understood. This gap in our knowledge has seriously limited our ability to manipulate hESC for therapeutic purposes.

In Eukaryotic cells, gene regulation depends on specific sequences in the DNA known as transcriptional regulatory elements. These regulatory DNA consists of promoters, enhancers, insulators and other regulatory sequences. As a key step towards understanding the gene regulatory mechanisms in hESC, we will produce a comprehensive map of promoters, enhancers and insulators in the hESC genome. We will use a newly developed, high throughput experimental strategy to identify these sequences that are engaged in gene activation in hESC. Our strategy involves identifying the DNA sequences that are associated with the specific transcription factors or chromatin modification signatures known to be present at each type of regulatory elements inside the hESC. We will use biochemical procedures to isolate these sequences from the cell and determine the resulting DNA in large scale with the use of DNA microarrays, containing of millions of DNA species that together represent the complete genomic makeup of the hESC. Completion of the proposed research is expected to improve our knowledge of the gene regulatory mechanisms in hESC, which in turn will facilitate the development of new strategies for stem cell based therapeutics.

Statement of Benefit to California:

Benefits to the State of California: Our research is aimed to provide a foundation for analysis of the mechanisms that control the production of stem cell proteins, which in turn would help us design new ways to manipulate the stem cells so that they can differentiate towards specified cell types. The knowledge base resulting from our research will directly support the effort by us and other California researchers to investigate the mechanisms of stem cell biology, and design new stem cell therapies.
